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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.45349 Seconds  
(without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-6

Perfect score: 583

Sequence: 1 MODWLTFQKKHLNTRDVC.....TECVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	95.4	104	1	RN30_RANPI
2	292	50.1	111	1	RNP0_RANCA
3	285.5	49.0	111	1	LECS_RANJA
4	269.5	46.2	111	1	RNP1_RANCA
5	149	25.6	119	1	RNP1_IGUG
6	131	22.5	124	1	RNP_GALMU
7	130.5	22.4	145	1	ANGR_MOUSE
8	130.5	22.4	146	1	ANGI_CERAE
9	128	22.0	148	1	ANGI_BOVIN
10	126	21.6	128	1	RNP_MYOCO
11	125	21.4	124	1	ANGI_BALAC
12	121.5	20.8	146	1	ANGI_MACMU
13	120	20.6	128	1	RNP_PROCU
14	119.5	20.5	145	1	ANGI_MOUSE
15	119	20.4	128	1	RNP_CAVPO
16	118.5	20.3	146	1	ANGI_PAPHA
17	117	20.1	124	1	RNP_CHIBR
18	116	19.9	125	1	ANGI_RABIT
19	116	19.9	128	1	RNP_HYDRY
20	114	19.6	124	1	ANGI_HIPAM
21	114	19.6	146	1	ANGI_MIOTA
22	113	19.4	147	1	ANGI_HUMAN
23	113	19.4	147	1	ANGI_PANTR
24	112	19.2	124	1	RNP_PIG
25	112	19.2	150	1	RNP_BOVIN
26	112	19.2	156	1	RNP_MYOG
27	111.5	19.1	147	1	RNP_HUMAN
28	111	19.0	128	1	RNP_HORSE
29	111	19.0	156	1	RNP_HYSCR
30	111	19.0	167	1	RNP_MOUSE
31	111	19.0	167	1	RNP_BOVIN
32	110.5	19.0	123	1	ANGI_PIG
33	110.5	19.0	155	1	ECPI_MOUSE

34	110	18.9	141	1	RNBR_GIRCA	O29542 giraffa cam
35	110	18.9	146	1	ANGI_SAGOE	O8wn62 saguinus oe
36	110	18.9	151	1	RNBR_AXIPR	P87350 axis porcin
37	109	18.7	123	1	ANG2_BOVIN	P80929 bos taurus
38	109	18.7	124	1	RNPA_CAVPO	P00678 cavia porce
39	109	18.7	124	1	RNP_AEPME	P07847 aepyceos m
40	109	18.7	124	1	RNP_ANTAM	P00668 antilocapra
41	109	18.7	124	1	RNP_SHEEP	P00661 ovis aries
42	109	18.7	146	1	ANGI_SATSC	O8wn60 salmifri sci
43	108.5	18.6	150	1	RNKG_SATSC	O46529 salmifri sci
44	108	18.5	124	1	RNP_BUBBU	P00657 bubalus bub
45	108	18.5	124	1	RNP_CONPA	P00660 connochaete

## ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	104 AA
AC	RN30_RANPI			
AC	P22069			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	P-30 Protein (EC 3.1.27.-) (Onconase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	3D-STRUCTURE MODELING.			
RC	TISSUE=Embryo;			
RC	MEDLINE=91093131; PubMed=1985896;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RC	MEDLINE=93066156; PubMed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;			
RA	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";			
RL	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RC	MEDLINE=9416079; PubMed=8120892;			
RA	Mosimann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC; 31-JAN-94.			
DR	InterPro: IPR001427; RnaseA.			
DR	Pfam: PF00074; RnaseA; 1.			
DR	Prodom: PD000535; RnaseA; 1.			
DR	SMART: SM00092; Rnase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.			
FT	MOD_RSS 1			
FT	ACT_SITE 10			
FT	ACT_SITE 31			
FT	ACT_SITE 31			
FT	ACT_SITE 97			
FT	DISULFID 19			
FT	DISULFID 30			
FT	DISULFID 75			
FT	DISULFID 90			

FT DISULFID 87 104  
 FT HELIX 3 10  
 FT STRAND 11 12  
 FT HELIX 19 22  
 FT TURN 23 24  
 FT TURN 26 30  
 FT STRAND 33 38  
 FT HELIX 41 48  
 FT TURN 49 50  
 FT STRAND 55 58  
 FT TURN 63 70  
 FT TURN 74 75  
 FT STRAND 77 84  
 FT STRAND 86 91  
 FT TURN 92 93  
 FT STRAND 94 101  
 SO SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 95.4%; Score 556; DB 1; Length 104;  
 Best Local Similarity 96.2%; Pred. No. 1.3e-52;  
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 61  
 DB 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKNVLT 60  
 QY 62 SEFYLSDCNVTSRPCCKYKLLKSKNTFCVTCENQAPVHFVGVGHC 105  
 DB 61 SEFYLSDCNVTSRPCCKYKLLKSKNTFCVTCENQAPVHFVGVGSC 104

RESULT 2  
 RNPO\_RANCA STANDARD; PRT; 111 AA.  
 AC P181916;

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).  
 OS Rana catesbeiana (Bull. frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Egg;  
 RX MEDLINE=67299649; PubMed=3304421;  
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;  
 RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";  
 RL Biochemistry 26:2189-2194(1987).  
 RN [2]  
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
 RX MEDLINE=92220613; PubMed=1373373;  
 RA Liao Y.-D.;  
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";  
 RL Nucleic Acids Res. 20:1371-1377(1992).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC TISSUE-Egg;  
 RX MEDLINE=93192604; PubMed=8448385;  
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H., Takayanagi Y., Hakomori S., Titani K.;  
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";  
 RL Glycobiology 3:37-45(1993).  
 RN [4]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=98437383; PubMed=9761686;  
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";  
 RL J. Mol. Biol. 283:231-244(1998).  
 CC -I- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.  
 CC -I- SUBUNIT: MONOMER.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: A27121; A27121.  
 DR PDB: 1BC4; 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_PC; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; lectin; 3D-structure.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SO SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 50.1%; Score 292; DB 1; Length 111;  
 Best Local Similarity 49.5%; Pred. No. 1.8e-24;  
 Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFTYSRPEPYKAICGIIASKN 57  
 DB 1 QMWATFOOKHLINPIINCMNTIMNIIYVGCKRVNTFTISSATVKAICTGVI-NMN 59  
 QY 58 VLTSEFYLSDC---NTSRPCCKYKLLKSKNTFCVTCENQAPVHFVGVGHC 105  
 DB 60 VLTSTRQLNCTRTSTTPPCPYSSRTETWICVCENQAPVHFAGIGRC 110

RESULT 3  
 LECS\_RANJA STANDARD; PRT; 111 AA.  
 AC P18839;

DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-).  
 OS Rana japonica (Japanese reddish frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8402;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=91035319; PubMed=2229005;  
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.";  
 RL J. Biochem. 108:139-143(1990).  
 CC -I- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -I- SUBUNIT: MONOMER.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0120; JX0120.

DR HSSP; P11916; IBC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNaseA: 1.  
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10  
 FT ACT\_SITE 35  
 FT ACT\_SITE 103  
 FT ACT\_SITE 103  
 FT DISULFID 19  
 FT DISULFID 34  
 FT DISULFID 52  
 FT DISULFID 94  
 FT DISULFID 111  
 SO SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.08; Score 285.5; DB 1; Length 111;  
 Best Local Similarity 45.08; Pred. No. 9.1e-24;  
 Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

OY 2 QDMULTFOCKHLTNRDVCNNIMSTNLF---HCKDKNTFLYSRPEPVKATCGIASKN 57  
 1 QNMAKFEKHIPTNSNTNCTIMDKSIYVGCKCKERTFTLISATTVKALCSGASTNRN 60  
 58 VLTTSSEYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPVHFVGVGHC 105  
 61 VLTSTRQNLNTCIRSATAPRCPYNSRTETNVICVCKENLPHVFAIGRC 111

DB 61 VLTSTRQNLNTCIRSATAPRCPYNSRTETNVICVCKENLPHVFAIGRC 111

RESULT 4  
 RNP\_LANCA STANDARD; PRT; 111 AA.  
 ID RNP\_LANCA  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull frog).  
 OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Mitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)  
 RT liver.";  
 FT J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP; P11916; IBC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNaseA: 1.  
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10  
 FT ACT\_SITE 35  
 FT ACT\_SITE 104  
 FT ACT\_SITE 104  
 FT DISULFID 19  
 FT DISULFID 34  
 FT DISULFID 52  
 FT DISULFID 94  
 FT DISULFID 111  
 SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.28; Score 269.5; DB 1; Length 111;  
 Best Local Similarity 43.28; Pred. No. 4.6e-22;  
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

OY 2 QDMULTFOCKHLTNRDVCNNIMSTNLF---HCKDKNTFLYSRPEPVKATCGIASKN 57  
 1 QNMAKFEKHIPTNSNTNCTIMDKSIYVGCKCKERTFTLISSEDDVVKALCSGASTNRN 60  
 58 VLTTSSEYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPVHFVGVGHC 105  
 61 ELSTTSFKLNTCIRDSITPRCPYHPSPDNNKICVCKEQLPHVFGIGKC 111

RESULT 5  
 RNP\_IGUG STANDARD; PRT; 119 AA.  
 ID RNP\_IGUG  
 AC P80287;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
 OS Iguana iguana (Common Iguana).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
 OX NCBI\_TaxID=8517;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94139745; PubMed=8307028;  
 RA Zhao W., Beintema J.J., Hofsteenge J.;  
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic  
 RT ribonuclease.";  
 FT Eur. J. Biochem. 219:641-646(1994).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP; P00656; ILSQ.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR PRINTS: PRO0794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNaseA: 1.  
 DR PROSITE: PS00127; RNaseA: PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1  
 FT DISULFID 25  
 FT DISULFID 39  
 FT DISULFID 57  
 FT DISULFID 10  
 FT ACT\_SITE 10  
 FT ACT\_SITE 40  
 FT ACT\_SITE 113  
 FT ACT\_SITE 113  
 SO SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 25.68; Score 149; DB 1; Length 119;  
 Best Local Similarity 30.78; Pred. No. 3.4e-09;  
 Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

OY 2 QDMULTFOCKHLTNRDVCNNIMSTNLFCKDKNTFLYSRPEPVKATCGIASKN 57  
 1 QDMSSFOCKHLDYETLSNNAVCGLDMQNRNLNLPKCKTRNFTVHASPSEIDQVCGSG 60  
 51 GIASKNVLTSF-FYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPVHF 99  
 61 GTHVEDNLVDSNESFDLTDCKNVGTAAPSCKYNGTGTKRIRIACENQPVHF 114

DB 61 GTHVEDNLVDSNESFDLTDCKNVGTAAPSCKYNGTGTKRIRIACENQPVHF 114

RESULT 6  
 RNP\_GALMU STANDARD; PRT; 124 AA.  
 ID RNP\_GALMU

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AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Galea musteloides (Cul's).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Galea.
OX NCBI_TaxID=10146;
RN [1]
RP SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and cul's ribonuclease."
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP: P00656; IRSN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 112 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA: 13870 MW: 60937E251A7BBA25 CXC64;

Query Match 22.5%; Score 131; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 3e-07;
Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

OY 5 LTPQKHL-----TNRDVCNNIM---STNLFHCKDKNTFYISRPVKAICKGIIA 54
DB 6 MKFQRHMDSDGHPDTNTN--YCNEMVRRSMTOGRCKPVTFFVHEPLEAVQAVC----S 59
OY 55 SKNV-----LTTSEFYLSDCNVTSRP---CKYELKSKTNTFCVTGEN--QAPVH 98
DB 60 QKNVPCKKNGQTCNQSHSMRTITDCRVTSSSKYPCSTRMTOAKSITIVACEGPPSVVH 119
OY 99 F 99
DB 120 F 120

RESULT 7
ANGL_MOUSE STANDARD: PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes."
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U22519; AAA91367.1; -
DR HSSP: P03950; IAAV.
DR MGD: MGI:104984; AngRP.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA: 16612 MW: 29A6EB814429C4AD CXC64;

Query Match 22.4%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 4e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

OY 31 CKDKNTFYISRPVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR-----PCYKILKS 83
DB 63 CKDVNTFTHDKNNIKAIKCGKSGPYGRNLKISRSFOVYCTHKGRSPRPCKIRASKG 122
OY 84 TTFECVTCENQAPVHF 99
DB 123 FRIYIGCENGMPVHF 138

RESULT 8
ANGL_CERAE STANDARD: PRT; 146 AA.
AC Q8WN66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution."

```

RL	MOL. BIOL. EVOL.	19:438-445(2002).
CC	- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,	
CC	ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAs (by similarity).	
CC	- SUBCELLULAR LOCATION: Secreted.	
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.	
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DR	EMBL; AF441664; AAL61646.1; -	
KW	Hydrolase; Nuclease; Endonuclease; Angiogenesis;	
RN	Protein synthesis inhibitor; Signal.	
FT	SIGNAL 1 24 BY SIMILARITY.	
FT	CHAIN 25 146 ANGIOGENIN.	
FT	MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).	
FT	ACT_SITE 37 37 BY SIMILARITY.	
FT	ACT_SITE 64 64 BY SIMILARITY.	
FT	ACT_SITE 138 138 BY SIMILARITY.	
FT	DISULFID 50 105 BY SIMILARITY.	
FT	DISULFID 63 116 BY SIMILARITY.	
FT	DISULFID 81 131 BY SIMILARITY.	
SO	SEQUENCE 146 AA; 16444 MW; 27860112E858DF9 CRC64;	
OY	Query Match 22.4%; Score 130.5; DB 1; Length 146; Best Local Similarity 30.7%; Pred. No. 4e-07;	
Db	Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;	
OY	6 TFQKHLLTRDYDCNNIMSTNFLFCRDKNTFYSRPRVKAIC--KGIASKNV-LTT 61 :::      53 TMRRRHLLTP-----CKDINFIGNHHRIKAIKAGDEGNPNRYGENTLRISK 97 :::	
OY	62 SEFLYLDCNVTS---RPCKIKLKKSNTPTFGVENCAPRVH 98   :::  :   ::  :	
Db	98 SPFOVTCNLKGSPRPCOYRATRGSRNIIVGENGDLRVH 138	
RESULT 9		
AC	ANGI_BOVIN STANDARD: PRT: 148 AA. P10152; Q9GKP9; 01-MAR-1989 (Rel. 10, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Angiogenin-1 precursor (EC 3.1.27.-). ANGI OR ANG. Bos taurus (bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. NCBI_TaxID=9913; RN NCB1_TaxID=9913; RN NCB1_TaxID=9913; RN NCB1_TaxID=9913; RP SEQUENCE FROM N.A. RC TISSUE=Liver; RA Chang S.-I.; RL "Cloning, sequencing, and expression of bovine angiogenin."; RN Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases. RP SEQUENCE OF 24-148. RC TISSUE=Milk; RX MEDLINE=89065101; PubMed=3197838; RA Maes P., Damatto D., Rommens C., Montreuil J., Spik G., Tartar A.; RT "The complete amino acid sequence of bovine milk angiogenin.";	

RN		FEBS Lett.241:41-45(1988).
RN	[3]	
RP	SEQUENCE OF 24-148.	
RC	TISSUE=Plasma;	
RX	MEDLINE=89375344; Pubmed=2775757;	
RA	Bond M.D., Strydom D.J.;	
RT	"Amino acid sequence of bovine angiogenin.";	
RL	Biochemistry 28:6110-6113(1989).	
RN	[4]	
RP	CHARACTERIZATION, AND SEQUENCE OF 25-55.	
RC	TISSUE=Plasma;	
RX	MEDLINE=89118214; Pubmed=3064806;	
RA	Bond M.D., Vallee B.L.;	
RT	"Isolation of bovine angiogenin using a placental ribonuclease inhibitor binding assay.";	
RL	Biochemistry 27:6282-6287(1988).	
RN	[5]	
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).	
RX	MEDLINE=95224057; Pubmed=7708754;	
RA	Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;	
RT	"Crystal structure of bovine angiogenin at 1.5-A resolution.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).	
RN	[6]	
RP	STRUCTURE BY NMR.	
RX	MEDLINE=96280645; Pubmed=8688423;	
RA	Leguin O., Albaret C., Boulens F., Spik G., Lallemand J.-Y.;	
RT	"Solution structure of bovine angiogenin by IH nuclear magnetic resonance spectroscopy.";	
RL	Biochemistry 35:8870-8880(1996).	
CC	-I- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONE BOUND, ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS; NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.	
CC	-I- SUBCELLULAR LOCATION: Secreted.	
CC	-I- TISSUE SPECIFICITY: SERUM, AND MILK.	
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to: license@isb-sib.ch)	
CC	-----	
DR	EMBL, AF135124; AAC47631.1; ..	
DR	PIR: A32474; A32474.	
DR	PDB: 1G10; 03-APR-96.	
DR	PDB: 1G10; 07-DEC-96.	
DR	InterPro: IPR001427; RNaseA.	
DR	Pfam: PF00074; RIBONUCLEASE.1.	
DR	PRINTS: PR00794; RIBONUCLEASE.	
DR	ProDom: PD000535; RNaseA.1.	
DR	SMART: SM00092; RNase_Pc.1.	
DR	PROSITE: PS00127; RNASE_PANCREATIC.1.	
KW	Hydrolase; Nuclease; Endonuclease; Angiogenesis; Protein synthesis inhibitor; Signal; 3D-structure.	
FT	SIGNAL	1 23
FT	CHAIN	24 148
FT	ACT_SITE	37
FT	ACT_SITE	64
FT	ACT_SITE	138
FT	DISULFID	50 105
FT	DISULFID	63 116
FT	DISULFID	81 131
SO	SEQUENCE	148 AA; B7999124CBB523DD CRC64;
Query Match	22.0%; Score 128; DB 1; Length 148;	
Best Local Similarity	34.0%; Pred. NO. 7.5e-07;	

Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

QY 17 DVDCKNTFTYSPREPYKAICKGIASKN-----VLTSTSEYL 66  
 DB 47 DEYCFNMKNRRLTRPCKDRNTFTHGKNDIKACE-----DRNQPTRGDLRIKSEFOI 102  
 QY 67 SDC---NVTGR-PCKYKALKSTNFCVTCENQAPVHF 99  
 DB 103 TICKHGSSRPCKRGATEDSRVIVGCEGCLPVHF 139

RESULT 10  
 RNP\_MYOCO  
 ID RNP\_MYOCO STANDARD; PRT; 128 AA.  
 AC P00676;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).  
 GN RNASEL OR RNSL.  
 OS Myocastor coypu (Coypu) (Nutria).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;  
 OC Myocastor.  
 NCBI\_TaxID=10157;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE-Pancreas;  
 RA MEDLINE=77065676; PubMed=999896;  
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;  
 RT "Isolation, properties and primary structure of coypu and chinchilla  
 pancreatic ribonuclease."  
 RL Biochem. Biophys. Acta 453:400-409(1976).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: A00822; NRCU.  
 DR HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR PRINTS: PR00794; RNaseA; 1.  
 DR PRODOM: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC...);  
 SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.6%; Score 126; DB 1; Length 128;  
 Best Local Similarity 29.9%; Pred. No. 1e-06;  
 Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 7 FQKHL-----TNRDVCNNIM-STNLF--HCKDKNTFTYSPREPYKAICKGIASKN 58  
 DB 8 FEROHMDSRGSPSTNPYCNEMKSRMTOGRCKPVTFFVHEPLADYQAVC-----FQKNV 63  
 QY 59 L-----TTFEFLSDCQNTSRP-----CKYKALKSTNFCVTCENQ--APVHF 99  
 DB 64 LCKNGOTNYQSSNMHITDCRVTNSDYPCSYRTSQEKSIVVACEGPNYVPHF 120

RESULT 11  
 RNP\_BALAC  
 ID RNP\_BALAC STANDARD; PRT; 124 AA.  
 AC P00673;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).  
 GN RNASEL OR RNSL.  
 OS Balaenoptera acutorostrata (minke whale) (lesser rorqual).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
 OC Balaenopteridae; Balaenoptera.  
 NCBI\_TaxID=9767;  
 RN (1)  
 RP SEQUENCE.  
 RC MEDLINE=76277855; PubMed=962870;  
 RA Emmens M., Welling G.W., Beintema J.J.;  
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic  
 ribonuclease."  
 RL Biochem. J. 157:317-323(1976).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: A00818; NRMK.  
 DR HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; rnaasea; 1.  
 DR PRINTS: PR00794; RNaseA; 1.  
 DR PRODOM: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 76 76 N-LINKED (GLCNAC...); IN 30% OF THE  
 MOLECULES.  
 SQ SEQUENCE 124 AA; 14125 MW; F57475459697E20 CRC64;

Query Match 21.4%; Score 125; DB 1; Length 124;  
 Best Local Similarity 28.6%; Pred. No. 1.3e-06;  
 Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 5 LTFQKHLTNRDVC-----CNNIMSTNLF--HCKDKNTFTYSPREPYKAICKGIASK 56  
 DB 6 MKFEROHMDSGNSPNNPNPCNMOMRRKMTQGRCKPVTFFVHESELEKYKAVC-----SK 61  
 QY 57 NVL-----TTFEFLSDCQNTSRP-----CKYKALKSTNFCVTCENQ--APVHF 99  
 DB 62 NVLCKNGTNCYESNHTWHTDCROTQSGSKYPNCAKYTSQREKHITVACGPNYVPHF 120

RESULT 12  
 ANGI\_MACMU  
 ID ANGI\_MACMU STANDARD; PRT; 146 AA.  
 AC Q8W63;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).  
 GN ANG OR RNASE5.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 NCBI\_TaxID=9544;  
 RN (1)



CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U22516; AAA91366.1; -  
DR PIR: A35932; A35932.  
DR HSSP: P03950; 1A4Y.  
DR MGD: MGI:88022; Ang.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaasea.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT CHAIN 1 24  
FT MOD\_RES 25 25 ANGIOGENIN.  
FT ACT\_SITE 37 37 PYRROLIDONE CARBOXYLIC ACID (BY  
FT ACT\_SITE 64 64 SIMILARITY).  
FT ACT\_SITE 137 137 BY SIMILARITY.  
FT DISULFID 50 104 BY SIMILARITY.  
FT DISULFID 63 115 BY SIMILARITY.  
FT DISULFID 81 130 BY SIMILARITY.  
SQ SEQUENCE 145 AA; 16228 MW; 06944260B8764938 CRC64;  
Query Match 20.5%; Score 119.5; DB 1; Length 145;  
Best Local Similarity 30.8%; Pred. No. 5.9e-06;  
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5;  
QY 10 KHLNTRDVD-----CNINSTNLF--HCKDKMTFTYSRPEPYKALC--KGIATSKN 57  
Db 32 KFLTONHDAKRGDRDRCYRMRKRSLSPTSCKDVMTFIGNKSNKAIKIGANGSPYREN 91  
QY 58 V-LITSEFYLSDCNVT-----RPCKYKLLKSTNTFCVTCENQAPVHF 99  
Db 92 LRMSKSPFOYTKHTGSGSPRCQYRASAGFRHVVIACENGLPVHF 138  
RESULT 15  
RNPB\_CAVPO STANDARD; PRT; 128 AA.  
ID RNPB\_CAVPO  
AC P00679;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pancreas;  
RX MEDLINE=77185023; PubMed=862624;  
RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastera W.,  
RA Beintema J.J.;  
RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary  
RT structure and glycosylation."  
RT Eur. J. Biochem. 75:91-100(1977).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
CC with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC PIR: A00826; NRGPB.  
DR HSSP: P00656; 1SRN.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaasea.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR PRODOM: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
FT DISULFID 26 84  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 72 BY SIMILARITY.  
FT ACT\_SITE 12 12 BY SIMILARITY.  
FT ACT\_SITE 41 41 BY SIMILARITY.  
FT ACT\_SITE 119 119 BY SIMILARITY.  
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).  
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).  
FT VARIANT 64 64 L -> P.  
SQ SEQUENCE 128 AA; 14406 MW; A2FA101A1A33E93B CRC64;  
Query Match 20.4%; Score 119; DB 1; Length 128;  
Best Local Similarity 28.3%; Pred. No. 5.8e-06;  
Matches 34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;  
QY 5 LTFQKKHL-----TNRDVCNNIM---STNLFHCKDKMTFTYSRPEPYKALCKGIATSKN 55  
Db 6 MKQROHMDREGSPSSNSN-CVNMIMRRMTGGRKPNVTFVHESLADYQAVC-----FQ 60  
QY 56 KNLV-----TTSEFYLSDCNVTSPR---CPYKLLKSTNTFCVTCENQ--APVHF 99  
Db 61 KNLCKNKGQTCNYQSVSRMRITDCAVTTSSSKFPNCVSRMSQAQKSIIVACEGDPVYVHF 120  
Search completed: June 25, 2003, 14:50:03  
Job time : 6.45349 secs